

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/846,017DATE: 03/04/98
TIME: 18:53:44

INPUT SET: S24002.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

#10
chh
6-4-98

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Cech, Thomas R.
6 Lingner, Joachim
7 Nakamura, Toru
8 Chapman, Karen B.
9 Morin, Gregg B.
10 Harley, Calvin
11 Andrews, William H.
12
13 (ii) TITLE OF INVENTION: Novel Telomerase
14
15 (iii) NUMBER OF SEQUENCES: 171
16
17 (iv) CORRESPONDENCE ADDRESS:
18 (A) ADDRESS: Townsend and Townsend and Crew LLP
19 (B) STREET: Two Embarcadero Center, 8th Floor
20 (C) CITY: San Francisco
21 (D) STATE: California
22 (E) COUNTRY: United States of America
23 (F) ZIP: 94111
24
25 (v) COMPUTER READABLE FORM:
26 (A) MEDIUM TYPE: Floppy disk
27 (B) COMPUTER: IBM PC compatible
28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
30
31 (vi) CURRENT APPLICATION DATA:
32 (A) APPLICATION NUMBER: US 08/846,017
33 (B) FILING DATE: 25-APR-1997
34 (C) CLASSIFICATION:
35
36 (vii) PRIOR APPLICATION DATA:
37 (A) APPLICATION NUMBER: US 08/844,419
38 (B) FILING DATE: 18-APR-1997
39 (C) CLASSIFICATION:
40
41 (vii) PRIOR APPLICATION DATA:
42 (A) APPLICATION NUMBER: US 08/724,643
43 (B) FILING DATE: 01-OCT-1996
44 (C) CLASSIFICATION:
45
46 (viii) ATTORNEY/AGENT INFORMATION:

RAW SEQUENCE LISTING
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47 (A) NAME: Apple, Randolph T.
48 (B) REGISTRATION NUMBER: 36,429
49 (C) REFERENCE/DOCKET NUMBER: 015389-002920US
50

51 (ix) TELECOMMUNICATION INFORMATION:
52 (A) TELEPHONE: (415) 576-0200
53 (B) TELEFAX: (415) 576-0300
54

55 (2) INFORMATION FOR SEQ ID NO:1:
56

57 (i) SEQUENCE CHARACTERISTICS:
58 (A) LENGTH: 3279 base pairs
59 (B) TYPE: nucleic acid
60 (C) STRANDEDNESS: single
61 (D) TOPOLOGY: linear
62

63 (ii) MOLECULE TYPE: other nucleic acid
64 (A) DESCRIPTION: /desc = "DNA"
65

66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
67

68	AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT AACCTCAGTA	60
69		
70	TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA ATGGAGGTTG ATGTTGATAA	120
71		
72	TCAAGCTGAT AATCATGGCA TTCACTCAGC TCTTAAGACT TGTGAAGAAA TTAAAGAAGC	180
73		
74	TAAAACGTTG TACTCTTGGA TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA	240
75		
76	TTATAAAGAT TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG	300
77		
78	AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT CAACTGGACT	360
79		
80	AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTCTT TCATCAAGCG ATGTTTCAGA	420
81		
82	TAGACAAAAA CTTCAATGAT TTGGATTTCA ACTTAAGGGA AATCAATTAG CAAAGACCCA	480
83		
84	TTTATTAACA GCTCTTTCAA CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT	540
85		
86	TAGAGCAATG ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA	600
87		
88	GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG ATCATTTGAA	660
89		
90	AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA GCAGACATGA ATGAACCTCG	720
91		
92	ATGTTGATCA ACCTGCAAAT ACAATGTCAA GAATGAGAAA GATCACTTTC TCAACAACAT	780
93		
94	CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT	840
95		
96	TAATAGAAAT AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT	900
97		
98	AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA GAATTAGAAA	960
99		

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100	GAAGCTAAAA	GATAAGGTTA	TCGAAAAAAT	TGCCTACATG	CTTGAGAAAAG	TCAAAGATTT	1020
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102	TAACTTCAAC	TACTATTTAA	CAAAATCTTG	TCCTCTTCCA	GAAAATTGGC	GGGAACGGAA	1080
103							
104	ACAAAAAATC	GAAAACTTGA	TAAATAAAAC	TAGAGAAGAA	AAGTCGAAGT	ACTATGAAGA	1140
105							
106	GCTGTTTAGC	TACACAACTG	ATAATAAATG	CGTCACACAA	TTTATTTAATG	AATTTTTCTA	1200
107							
108	CAATATACTC	CCCAAAGACT	TTTTGACTGG	AAGAAACCGT	AAGAATTTTC	AAAAGAAAGT	1260
109							
110	TAAGAAATAT	GTGGAACATA	ACAAGCATGA	ACTCATTAC	AAAACTTAT	TGCTTGAGAA	1320
111							
112	GATCAATACA	AGAGAAATAT	CATGGATGCA	GGTTGAGACC	TCTGCAAAGC	ATTTTTATTA	1380
113							
114	TTTTGATCAC	GAAAAACATCT	ACGTCTTATG	GAAATTGCTC	CGATGGATAT	TCGAGGATCT	1440
115							
116	CGTCGTCTCG	CTGATTAGAT	GATTTTTCTA	TGTCACCGAG	CAACAGAAAA	GTTACTCCAA	1500
117							
118	AACCTATTAC	TACAGAAAAG	ATATTTGGGA	CGTCATTATG	AAAATGTCAA	TCGCAGACTT	1560
119							
120	AAAGAAGGAA	ACGCTTGCTG	AGGTCCAAGA	AAAAGAGGTT	GAAGAATGGA	AAAAGTCGCT	1620
121							
122	TGGATTTGCA	CCTGGAAAAC	TCAGACTAAT	ACCGAAGAAA	ACTACTTTCC	GTCCAATTAT	1680
123							
124	GACTTTCAAT	AAGAAGATTG	TAAATTCAGA	CCGGAAGACT	ACAAAATTAA	CTACAAATAC	1740
125							
126	GAAGTTATTG	AACTCTCACT	TAATGCTTAA	GACATTGAAG	AATAGAATGT	TTAAAGATCC	1800
127							
128	TTTTGGATTG	GCTGTTTTTA	ACTATGATGA	TGTAATGAAA	AAGTATGAGG	AGTTTGTTTG	1860
129							
130	CAAATGGAAG	CAAGTTGGAC	AACCAAAACT	CTTCTTTGCA	ACTATGGATA	TCGAAAAGTG	1920
131							
132	ATATGATAGT	GTAAACAGAG	AAAACTATC	AACATTCCCTA	AAAAC'TACTA	AATTACTTTC	1980
133							
134	TTCAGATTTC	TGGATTATGA	CTGCACAAAT	TCTAAAGAGA	AAGAATAACA	TAGTTATCGA	2040
135							
136	TTGAAAAAAC	TTTAGAAAAG	AAGAAATGAA	AGATTATTTT	AGACAGAAAT	TCCAGAAGAT	2100
137							
138	TGCACTTGAA	GGAGGACAAT	ATCCAACCTT	ATTGAGTGTT	CTTGAAAATG	AACAAAATGA	2160
139							
140	CTTAAATGCA	AAGAAAACAT	TAATTGTTGA	AGCAAAGCAA	AGAAATTATT	TTAAGAAAGA	2220
141							
142	TAACTTACTT	CAACCAGTCA	TTAATATTTG	CCAATATAAT	TACATTAAC	TTAATGGGAA	2280
143							
144	GTTTTATAAA	CAAACAAAAG	GAATTCCTCA	AGGTCTTTGA	GTTTCATCAA	TTTTGTCATC	2340
145							
146	ATTTTATTAT	GCAACATTAG	AGGAAAGCTC	CTTAGGATTC	CTTAGAGATG	AATCAATGAA	2400
147							
148	CCCTGAAAAT	CCAAATGTTA	ATCTTCTAAT	GAGACTTACA	GATGACTATC	TTTTGATTAC	2460
149							
150	AACTCAAGAG	AATAATGCAG	TATTGTTTAT	TGAGAACTT	ATAAACGTAA	GTCGTGAAAA	2520
151							
152	TGGATTTAAA	TTCAATATGA	AGAAACTACA	GACTAGTTTT	CCATTAAGTC	CAAGCAAATT	2580

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153
154 TGCAAAATAC GGAATGGATA GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG 2640
155
156 GATTGGCATC TCAATTGATA TGAAAACCTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT 2700
157
158 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT CAATGTGGCT 2760
159
160 CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC CATTATTTTA GAAAGACGAT 2820
161
162 TACAACCGAA GACTTTGCGA ATAAAACCTCT CAACAAGTTA TTTATATCAG GCGGTTACAA 2880
163
164 ATACATGCAA TGAGCCAAAG AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG 2940
165
166 TATGATCGAC TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA 3000
167
168 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG ACTTTTTCCT 3060
169
170 TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA AAGTACATTT TCAACAGAGT 3120
171
172 TTGCATGATC CTCAAGGCAA AAGAAGCAAA GCTAAAAAGT GACCAATGTC AATCTCTAAT 3180
173
174 TCAATATGAT GCATAGTCGA CTATTCTAAC TTATTTTGGG AAGTTAATTT TCAATTTTTG 3240
175
176 TCTTATATAC TGGGGTTTTG GGGTTTTGGG GTTTTGGGG 3279
177

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: Not Relevant
(D) TOPOLOGY: Not Relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

190 Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
191 1 5 10 15
192
193 Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
194 20 25 30
195
196 Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
197 35 40 45
198
199 Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
200 50 55 60
201
202 Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys
203 65 70 75 80
204
205 Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu

RAW SEQUENCE LISTING PATENT APPLICATION US/08/846,017

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	85	90	95
206			
207			
208	Val Glu Leu Leu Ser Ser Ser Asp	Val Ser Asp Arg Gln Lys Leu Gln	
209	100	105	110
210			
211	Cys Phe Gly Phe Gln Leu Lys Gly	Asn Gln Leu Ala Lys Thr His Leu	
212	115	120	125
213			
214	Leu Thr Ala Leu Ser Thr Gln Lys	Gln Tyr Phe Phe Gln Asp Glu Trp	
215	130	135	140
216			
217	Asn Gln Val Arg Ala Met Ile Gly	Asn Glu Leu Phe Arg His Leu Tyr	
218	145	150	155
219			
220	Thr Lys Tyr Leu Ile Phe Gln Arg	Thr Ser Glu Gly Thr Leu Val Gln	
221	165	170	175
222			
223	Phe Cys Gly Asn Asn Val Phe Asp	His Leu Lys Val Asn Asp Lys Phe	
224	180	185	190
225			
226	Asp Lys Lys Gln Lys Gly Gly Ala	Ala Asp Met Asn Glu Pro Arg Cys	
227	195	200	205
228			
229	Cys Ser Thr Cys Lys Tyr Asn Val	Lys Asn Glu Lys Asp His Phe Leu	
230	210	215	220
231			
232	Asn Asn Ile Asn Val Pro Asn Trp	Asn Asn Met Lys Ser Arg Thr Arg	
233	225	230	235
234			
235	Ile Phe Tyr Cys Thr His Phe Asn	Arg Asn Asn Gln Phe Phe Lys Lys	
236	245	250	255
237			
238	His Glu Phe Val Ser Asn Lys Asn	Asn Ile Ser Ala Met Asp Arg Ala	
239	260	265	270
240			
241	Gln Thr Ile Phe Thr Asn Ile Phe	Arg Phe Asn Arg Ile Arg Lys Lys	
242	275	280	285
243			
244	Leu Lys Asp Lys Val Ile Glu Lys	Ile Ala Tyr Met Leu Glu Lys Val	
245	290	295	300
246			
247	Lys Asp Phe Asn Phe Asn Tyr Tyr	Leu Thr Lys Ser Cys Pro Leu Pro	
248	305	310	315
249			
250	Glu Asn Trp Arg Glu Arg Lys Gln	Lys Ile Glu Asn Leu Ile Asn Lys	
251	325	330	335
252			
253	Thr Arg Glu Glu Lys Ser Lys Tyr	Tyr Glu Glu Leu Phe Ser Tyr Thr	
254	340	345	350
255			
256	Thr Asp Asn Lys Cys Val Thr Gln	Phe Ile Asn Glu Phe Phe Tyr Asn	
257	355	360	365
258			

PAGE: 1

SEQUENCE VERIFICATION REPORT
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Original Text

Application No.:

08/846017

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

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